



SEQUENCE LISTING

<10> Hall, Roderick L.
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<120> Method For Accelerating The Rate of Mucociliary Clearance

<130> 98-736-A

<140> US 09/441,966

<141> 1999-11-17

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<160> 105

<170> PatentIn version 3.1

<210> 1

<211> 179

<212> PRT

<213> Homo sapiens

<400> 1

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
1 5 10 15

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg

115

120

125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
130 135 140

Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
165 170 175

Ala Val Ser

<210> 2
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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)..(18)
<223>

<400> 2

Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
1 5 10 15

Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
20 25 30

Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
35 40 45

Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
50 55 60

Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
65 70 75 80

Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
85 90 95

Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp

100

105

110

His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
115 120 125

Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
130 135 140

Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
145 150 155 160

Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
165 170 175

Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
180 185 190

Ala Gly Ala Val Ser
195

<210> 3
<211> 153
<212> PRT
<213> Homo sapiens

<400> 3

Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
1 5 10 15

Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
20 25 30

Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
35 40 45

Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly
50 55 60

Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala
65 70 75 80

Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr
85 90 95

Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser
100 105 110

Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe
115 120 125

Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu
130 135 140

Ala Cys Met Leu Arg Cys Phe Arg Gln
145 150

<210> 4
<211> 58
<212> PRT
<213> Homo sapiens

<400> 4

Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
1 5 10 15

Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
20 25 30

Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
35 40 45

Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
50 55

<210> 5
<211> 51
<212> PRT
<213> Homo sapiens

<400> 5

Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
1 5 10 15

Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
20 25 30

Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
35 40 45

Lys Lys Cys
50

<210> 6
<211> 58
<212> PRT
<213> Homo sapiens

<400> 6

Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
1 5 10 15

Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
20 25 30

Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
35 40 45

Glu Ala Cys Met Leu Arg Cys Phe Arg Gln
50 55

<210> 7
<211> 51
<212> PRT
<213> Homo sapiens

<400> 7

Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
1 5 10 15

Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
20 25 30

Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
35 40 45

Leu Arg Cys
50

<210> 8
<211> 92
<212> PRT
<213> Homo sapiens

<400> 8

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
1 5 10 15

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
85 90

<210> 9

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Consensus DNA sequence of human Bikunin (Fig. 3).

<220>

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<222> (679)..(679)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (707)..(707)

<223> "n" is any nucleotide.

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ccgagaacgc agcatccacg acttctgcct ggtgtgaag gtggtgggca gatgccgggc 120

ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg 180

gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc 240

cactgtcaca gagaatgcca cgggtgacct ggccaccagc aggaatgcag cggattcctc 300

tgtcccaagt gctcccagaa ggcaggatct tgaagaccac tccagcgata tgttcaacta 360
 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcacact tcccacgtg 420
 gtactttgac gtggagagga actcctgcaa taacttcac tatggaggct gccggggcaa 480
 taagaacagc taccgctctg aggaggcctg catgctccgc tgcttccgcc agcaggagaa 540
 tctctccctg ccccttgggt caaaggtggg ggttctggcc ggggctgttt cgtgatgggt 600
 ttgatccttt tctggggag catccatggg ctactgatt ccgggtggca aggaggaacc 660
 aggagcgtgc cctgcgganc gtctggagct tcggagatga caaggnt 708

<210> 10
 <211> 197
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acids -18 to 179 of translation of consensus sequence in Fig. 3.
 <400> 10

Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
 1 5 10 15

Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
 20 25 30

Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
 35 40 45

Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
 50 55 60

Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
 65 70 75 80

Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
 85 90 95

Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
 100 105 110

His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
 115 120 125

Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
130 135 140

Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
145 150 155 160

Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
165 170 175

Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
180 185 190

Ala Gly Ala Val Ser
195

<210> 11
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Variants of human Bikunin.

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE

<222> (21)..(26)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (42)..(42)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (45)..(47)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (52)..(52)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (64)..(64)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (103)..(103)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa"

in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (112)..(112)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

But Bc
<220>
<221> MISC_FEATURE
<222> (116)..(121)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

Q5 Cont
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<222> (135)..(135)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (137)..(137)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
<221> MISC_FEATURE
<222> (140)..(142)
<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
 <221> MISC_FEATURE
 <222> (147)..(147)
 <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>
 <221> MISC_FEATURE
 <222> (159)..(159)
 <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<400> 11

Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val
 1 5 10 15

Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr
 20 25 30

Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser
 35 40 45

Asn Asn Tyr Xaa Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Xaa
 50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ser Thr Ser Arg Asn Ala Ala Asp
 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu His Asp Ser
 85 90 95

Ser Asp Met Phe Asn Tyr Xaa Glu Tyr Cys Thr Ala Asn Ala Val Xaa
 100 105 110

Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Tyr Phe Asp Val Glu Arg
 115 120 125

Asn Ser Cys Asn Asn Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Lys Asn
 130 135 140

Ser Tyr Xaa Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Xaa Gln
145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
165 170 175

Ala Val Ser

<210> 12
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (361)..(361)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (367)..(367)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (384)..(384)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (390)..(390)
<223> "n" is any nucleotide.

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ggccgggtcg tttctgcct ggctgggatc gctgctctc tctgggggtcc tggccggccg 60
accgagaacg cagcatccac gacttctgcc tgggtgtcgaa ggtggtgggc agattccggg 120
cctccatgcc taggtggtgg tacaatgtca ctgacggatc ctgccagctg tttgtgtatg 180
ggggctgtga cggaacagc aataattacc tgaccaagga ggagtgcctc aagaaatgtg 240
ccactgtcac agagaatgcc acgggtgacc tggccaccag caggaatgca gcggattcct 300
ctgtcccaag tgctccaga aggcaggatt cttgaagacc acttcagcga tatgtttcaa 360
ntattgnaag aataattgca ccgnaacgn att 393

<210> 13
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)..(18)
<223>

<400> 13

Pro Gly Arg Phe Ser Pro Gly Trp Asp Arg Cys Ser Ser Leu Gly Ser
1 5 10 15

Trp Pro Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
20 25 30

Lys Val Val Gly Arg Glu Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
35 40 45

Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
50 55 60

Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
65 70 75 80

Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
85 90 95

Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
100 105 110

<210> 14
<211> 510
<212> DNA
<213> Homo sapiens

<220>
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<222> (424)..(424)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (481)..(481)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (509)..(509)
<223> "n" is any nucleotide.

<400> 14
gcaataatta cctgaccaag gaggagtgcc tcaagaaatg tgccactgtc acagagaatg 60
ccacgggtga cctggccacc agcaggaatg cagcggattc ctctgtccca agtctcccag 120
aaggcaggat tctgaagacc actccagcga tatgttcaac tatgaagaat actgcaccgc 180
caacgcagtc actgggcctt gccgtgcac cttcccacgc tggactttg acgtggagag 240
gaactcctgc aataacttca tctatggagg ctgccggggc aataagaaca gctaccgctc 300
tgaggaggcc tgcattgtcc gctgcttccg ccagcaggag aatcctcccc tgccccttgg 360
ctcaaaggtg gtgggttctgg ccggggctgt ttctgtatgg tgttgatcct tttctggggg 420
agcntccatg gtcttactga ttccgggtgg caaggaggaa ccaggagcgt gccctgcgga 480
ncgtctggag cttcggagat gacaaggnt 510

<210> 15
<211> 20
<212> PRT
<213> Homo sapiens

<400> 15
Leu Pro Asp Gln Gly Gly Val Pro Gln Glu Met Cys His Cys His Arg
1 5 10 15

Glu Cys His Gly
20

<210> 16
<211> 427
<212> DNA
<213> Homo sapiens

<220>
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<222> (3)..(3)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (11)..(12)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (17)..(17)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (48)..(48)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (425)..(425)
<223> "n" is any nucleotide.

Sub B6

<400> 16
gngcgcggtt nntcgcntgc tgggatcgct gcacctctct ggggtcgngg cggccgaccg 60
agaacgcagc atccacgact tctgcctggt gtcgaagggt gtgggcagat gccgggcctc 120
catgcctagg tgggtggtaca atgtcactga cggatcctgc cagctgtttg tgtatggggg 180
ctgtgacgga aacagcaata attacctgac caaggaggag tgcctcaaga aatgtgccac 240
tgtcacagag aatgccacgg gtgacctggc caccagcagg aatgcagcgg attcctctgt 300
cccaagtgtc ccagaaggc aggattctga agaccactcc agcgatatgt tcaactatga 360
*95
Cont* agaatactgg caccgccaac gcattcactg ggcttgcgtg catccttccc acgctgggtac 420
tttgncg 427

<210> 17
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (6)..(6)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (401)..(401)
<223> "n" is any nucleotide.

<220>
<221> misc_feature

<222> (407)..(407)
<223> "n" is any nucleotide.

<400> 17
tgggantcgc tgctcctctc tggggctctg gcggccgacc gagaacgcag catccacgac 60
ttctgcctgg tgtcgaaggt ggtgggcaga tgccgggcct ccatgcctag gtggtggtac 120
aatgtcactg acggatcctg ccagctgttt gtgtatgggg gctgtgacgg aaacagcaat 180
aattacctga ccaaggagga gtgcctcaag aaatgtgcca ctgtcacaga gaatgccacg 240
ggtgacctgg ccaccagcag gaatgcagcg gattcctctg tcccaagtgc tcccagaagg 300
caggattctg aagaccactc cagcgatatg ttcaactatg aagaatactg caccgccaac 360
gcagtcactg ggccttgcgt ggaatccttt cccacgctgg naatttngac gttgagaagg 420
aac 423

But B67
<210> 18
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of tissue factor pathway inhibitor precursor 1.

<400> 18
His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys Ala Ile
1 5 10 15

95 Cont.
Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe
20 25 30

Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu
35 40 45

Glu Cys Lys Lys Met Cys Thr Arg Asp
50 55

<210> 19
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of tissue factor pathway inhibitor precursor 1.

<400> 19

Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr
1 5 10 15

Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe
20 25 30

Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu
35 40 45

Glu Cys Lys Asn Ile Cys Glu Asp Gly
50 55

<210> 20
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of tissue factor pathway inhibitor precursor.
<400> 20

Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn
1 5 10 15

Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe
20 25 30

Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln
35 40 45

Glu Cys Leu Arg Ala Cys Lys Lys Gly
50 55

<210> 21
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of tissue factor pathway inhibitor precursor 2.
<400> 21

Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
1 5 10 15

Leu Leu Arg Tyr Tyr Tyr Arg Tyr Arg Thr Gln Ser Cys Arg Gln Phe
20 25 30

Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
35 40 45

Ala Cys Asp Asp Ala Cys Trp Arg Ile
50 55

<210> 22
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of tissue factor pathway inhibitor precursor 2.

<400> 22

Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn
1 5 10 15

Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe
20 25 30

Thr Tyr Thr Gly Cys Gly Asn Asn Asp Asn Asn Phe Val Ser Arg Glu
35 40 45

Asp Ser Lys Arg Ala Cys Ala Lys Ala
50 55

<210> 23
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of amyloid precursor protein homologue.

<400> 23

Lys Ala Val Cys Ser Gln Glu Ala Met Thr Gly Pro Cys Arg Ala Val
1 5 10 15

Met Pro Arg Thr Thr Phe Asp Leu Ser Lys Gly Lys Cys Val Arg Phe
20 25 30

Ile Thr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Glu Ser Glu Asp

35

40

45

Tyr Cys Met Ala Val Cys Lys Ala Met
50 55

<210> 24
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of aprotinin.

<400> 24

Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Lys Ala
1 5 10 15

Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
20 25 30

Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys Ser Ala
35 40 45

Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
50 55

<210> 25
<211> 51
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.

<400> 25

Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys Met Gly Met Thr Ser Arg
1 5 10 15

Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys Glu Thr Phe Gln Tyr Gly
20 25 30

Gly Cys Met Gly Asn Gly Asn Asn Phe Val Thr Glu Lys Glu Cys Leu
35 40 45

Gln Thr Cys
50

<210> 26
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.

<400> 26

Val Ala Ala Cys Asn Leu Pro Ile Val Arg Gly Pro Cys Arg Ala Phe
1 5 10 15

Ile Gln Leu Trp Ala Phe Asp Ala Val Lys Gly Lys Cys Val Leu Phe
20 25 30

Pro Tyr Gly Gly Cys Gln Gly Asn Gly Asn Lys Phe Tyr Ser Glu Lys
35 40 45

Glu Cys Arg Glu Tyr Cys Gly Val Pro
50 55

<210> 27
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Kunitz-like domain of amyloid precursor protein.

<400> 27

Glu Val Cys Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met
1 5 10 15

Ile Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe
20 25 30

Phe Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu
35 40 45

Tyr Cys Met Ala Val Cys Gly Ser Ala
50 55

<210> 28
<211> 51
<212> PRT

<213> Unknown

<220>

<223> Kunitz-like domain of collagen alpha-3(VI) precursor.

<400> 28

Cys Lys Leu Pro Lys Asp Glu Gly Thr Cys Arg Asp Phe Ile Leu Lys
1 5 10 15

Trp Tyr Tyr Asp Pro Asn Thr Lys Ser Cys Ala Arg Phe Trp Tyr Gly
20 25 30

Gly Cys Gly Gly Asn Glu Asn Lys Phe Gly Ser Gln Lys Glu Cys Glu
35 40 45

Lys Val Cys
50

<210> 29

<211> 57

<212> PRT

<213> Unknown

<220>

<223> Kunitz-like domain of HKI-B9.

<400> 29

Pro Asn Val Cys Ala Phe Pro Met Glu Lys Gly Pro Cys Gln Thr Tyr
1 5 10 15

Met Thr Arg Trp Phe Phe Asn Phe Glu Thr Gly Glu Cys Glu Leu Phe
20 25 30

Ala Tyr Gly Gly Cys Gly Gly Asn Ser Asn Asn Phe Leu Arg Lys Glu
35 40 45

Lys Cys Glu Lys Phe Cys Lys Phe Thr
50 55

<210> 30

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' sense oligonucleotide used in Example 6.

<400> 30
gccaaagcttg gataaaagat atgaagaata ctgcaccgcc aacgca 46

<210> 31
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' antisense oligonucleotide used in Example 6.

<400> 31
ggggatcctc actgctggcg gaagcagcgg agcat 35

<210> 32
<211> 206
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloned bikunin cDNA fragment in Example 6.

<400> 32
ccaagcttgg ataaaagata tgaagaatac tgcaccgcc aacgagtcac tgggccttgc 60
cgtgcatcct tcccacgctg gtactttgac gtggagagga actcctgcaa taacttcac 120
tatggaggct gccggggcaa taagaacagc taccgctctg aggaggcctg catgctccgc 180
tgcttccgcc agcagtgagg atcccc 206

<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' PCR primer used to amplify EST R74593.

<400> 33
cgaagcttca tctccgaagc tccagacg 28

<210> 34
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' PCR primer used to amplify EST R74593.

<400> 34
aggatctaga caataattac ctgaccaagg a 31

<210> 35
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' PCR primer used to amplify EST R35464.

<400> 35
ggtctagagg ccgggtccgt ttctcgctg gctggga 37

<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' PCR primer used to amplify EST R34808.

<400> 36
cacctgatcg cgagacccc 19

Ref-BL
<210> 37
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector specific DNA sequencing primer (SP6).

<400> 37
gatttaggtg acactatag 19

Q5
Cont
<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector specific DNA sequencing primer (T7).

<400> 38
taatacgact cactataggg 20

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene specific DNA sequencing primer.

<400> 39
ttacctgacc aaggaggagt gc 22

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene specific DNA sequencing primer.

<400> 40
aatccgctgc attcctgctg gtg 23

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene specific DNA sequencing primer.

<400> 41
cagtcactgg gccttgccgt 20

<210> 42
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' sense oligonucleotide used in Example 5.

<400> 42
gaaggggtaa gcttggataa aagatatgaa gaatactgca ccgccaacgc agtcactggg 60

ccttgccgtg catccttccc acgctggtac tttgacgtgg agagg 105

<210> 43
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' antisense oligonucleotide used in Example 5.

<400> 43
cgcggatccc tactggcgga agcagcggag catgcaggcc tcctcagagc ggtagctgtt 60

cttattgccc cggcagcctc catagatgaa gttattgcag gagttcctct ccacgtcaaa 120

gtaccagcg 129

<210> 44
<211> 207
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloned bikunin fragment in Example 5.

<400> 44
gaaggggtaa gcttggataa aagatatgaa gaatactgca ccgccaacgc agtcactggg 60
ccttgccgtg catccttccc acgctggtac ttgacgtgg agaggaactc ctgcaataac 120
ttcatctatg gaggctgccc gggcaataag aacagctacc gctctgagga ggctgcatg 180
ctccgctgct tccgccagta gggatcc 207

<210> 45
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> EST derived consensus sequence of human Bikunin (Figs. 4D and 4G).

<220>
<221> SIGNAL
<222> (1)..(23)
<223>

<400> 45

Met Leu Arg Ala Glu Ala Asp Gly Val Ser Arg Leu Leu Gly Ser Leu
1 5 10 15

Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp
20 25 30

Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro
35 40 45

Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr
50 55 60

Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys
65 70 75 80

Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala
85 90 95

Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg
100 105 110

Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr
115 120 125

Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
130 135 140

Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
145 150 155 160

Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
165 170 175

Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser
180 185 190

Lys Val Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe
195 200 205

Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln
210 215 220

Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln
225 230 235 240

Leu Val Lys Asn Thr Tyr Val Leu
245

<210> 46
<211> 782
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (61)..(780)
<223>

<400> 46
acctgatcgc gagaccccaa cggctgggtgg cgctgcctgc gcgtctcggc tgagctggcc 60
atg gcg cag ctg tgc ggg ctg agg cgg agc cgg gcg ttt ctc gcc ctg 108

Met	Ala	Gln	Leu	Cys	Gly	Leu	Arg	Arg	Ser	Arg	Ala	Phe	Leu	Ala	Leu		
1				5					10					15			
ctg	gga	tcg	ctg	ctc	ctc	tct	ggg	gtc	ctg	gcg	gcc	gac	cga	gaa	cgc		156
Leu	Gly	Ser	Leu	Leu	Leu	Ser	Gly	Val	Leu	Ala	Ala	Asp	Arg	Glu	Arg		
			20					25					30				
agc	atc	cac	gac	ttc	tgc	ctg	gtg	tcg	aag	gtg	gtg	ggc	aga	tgc	cgg		204
Ser	Ile	His	Asp	Phe	Cys	Leu	Val	Ser	Lys	Val	Val	Gly	Arg	Cys	Arg		
		35						40				45					
gcc	tcc	atg	cct	agg	tgg	tgg	tac	aat	gtc	act	gac	gga	tcc	tgc	cag		252
Ala	Ser	Met	Pro	Arg	Trp	Trp	Tyr	Asn	Val	Thr	Asp	Gly	Ser	Cys	Gln		
	50					55					60						
ctg	ttt	gtg	tat	ggg	ggc	tgt	gac	gga	aac	agc	aat	aat	tac	ctg	acc		300
Leu	Phe	Val	Tyr	Gly	Gly	Cys	Asp	Gly	Asn	Ser	Asn	Asn	Tyr	Leu	Thr		
65					70					75					80		
aag	gag	gag	tgc	ctc	aag	aaa	tgt	gcc	act	gtc	aca	gag	aat	gcc	acg		348
Lys	Glu	Glu	Cys	Leu	Lys	Lys	Cys	Ala	Thr	Val	Thr	Glu	Asn	Ala	Thr		
			85						90					95			
ggt	gac	ctg	gcc	acc	agc	agg	aat	gca	gcg	gat	tcc	tct	gtc	cca	agt		396
Gly	Asp	Leu	Ala	Thr	Ser	Arg	Asn	Ala	Ala	Asp	Ser	Ser	Val	Pro	Ser		
			100					105					110				
gct	ccc	aga	agg	cag	gat	tct	gaa	gac	cac	tcc	agc	gat	atg	ttc	aac		444
Ala	Pro	Arg	Arg	Gln	Asp	Ser	Glu	Asp	His	Ser	Ser	Asp	Met	Phe	Asn		
			115					120				125					
tat	gaa	gaa	tac	tgc	acc	gcc	aac	gca	gtc	act	ggg	cct	tgc	cgt	gca		492
Tyr	Glu	Glu	Tyr	Cys	Thr	Ala	Asn	Ala	Val	Thr	Gly	Pro	Cys	Arg	Ala		
	130					135					140						
tcc	ttc	cca	cgc	tgg	tac	ttt	gac	gtg	gag	agg	aac	tcc	tgc	aat	aac		540
Ser	Phe	Pro	Arg	Trp	Tyr	Phe	Asp	Val	Glu	Arg	Asn	Ser	Cys	Asn	Asn		
	145				150					155					160		
ttc	atc	tat	gga	ggc	tgc	cgg	ggc	aat	aag	aac	agc	tac	cgc	tct	gag		588
Phe	Ile	Tyr	Gly	Gly	Cys	Arg	Gly	Asn	Lys	Asn	Ser	Tyr	Arg	Ser	Glu		
			165					170						175			
gag	gcc	tgc	atg	ctc	cgc	tgc	ttc	cgc	cag	cag	gag	aat	cct	ccc	ctg		636
Glu	Ala	Cys	Met	Leu	Arg	Cys	Phe	Arg	Gln	Gln	Glu	Asn	Pro	Pro	Leu		
			180					185					190				
ccc	ctt	ggc	tca	aag	gtg	gtg	gtt	ctg	gcg	ggg	ctg	ttc	gtg	atg	gtg		684
Pro	Leu	Gly	Ser	Lys	Val	Val	Val	Leu	Ala	Gly	Leu	Phe	Val	Met	Val		
		195					200					205					
ttg	atc	ctc	ttc	ctg	gga	gcc	tcc	atg	gtc	tac	ctg	atc	cgg	gtg	gca		732
Leu	Ile	Leu	Phe	Leu	Gly	Ala	Ser	Met	Val	Tyr	Leu	Ile	Arg	Val	Ala		
	210					215					220						
cgg	agg	aac	cag	gag	cgt	gcc	ctg	cgc	acc	gtc	tgg	agc	ttc	gga	gat		780
Arg	Arg	Asn	Gln	Glu	Arg	Ala	Leu	Arg	Thr	Val	Trp	Ser	Phe	Gly	Asp		

225

230

235

240

ga

782

<210> 47
 <211> 240
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)..(27)
 <223>

<400> 47

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu
 1 5 10 15

Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg
 20 25 30

Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg
 35 40 45

Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln
 50 55 60

Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr
 65 70 75 80

Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr
 85 90 95

Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser
 100 105 110

Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn
 115 120 125

Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
 130 135 140

Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
 145 150 155 160

Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
165 170 175

Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu
180 185 190

Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly Leu Phe Val Met Val
195 200 205

Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala
210 215 220

Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Phe Gly Asp
225 230 235 240

<210> 48
<211> 1544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1358)..(1358)
<223> "n" is any nucleotide.

<220>
<221> exon
<222> (301)..(1056)
<223>

<400> 48
gcacgagttg ggaggtgtag cgcggctctg aacgcgctga gggccgttga gtgtcgcagg 60
cggcgagggc gcgagtgagg agcagaccca ggcatcgcgc gccgagaagg cggggcgctcc 120
ccacactgaa ggtccgga aa ggcgacttcc gggggctttg gcacctggcg gaccctcccg 180
gagcgtcggc acctgaacgc gaggcgctcc attgcgcgtg cgcgttgagg ggcttcccg 240
acctgatcgc gagaccccaa cggctggtgg cgtcgctcgc gcgtctcggc tgagctggcc 300
atg gcg cag ctg tgc ggg ctg agg cgg agc cgg gcg ttt ctc gcc ctg 348
Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu
1 5 10 15
ctg gga tcg ctg ctc ctc tct ggg gtc ctg gcg gcc gac cga gaa cgc 396
Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg
20 25 30

agc atc cac gac ttc tgc ctg gtg tgc aag gtg gtg ggc aga tgc cgg 444
 Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg
 35 40 45

gcc tcc atg cct agg tgg tgg tac aat gtc act gac gga tcc tgc cag 492
 Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln
 50 55 60

ctg ttt gtg tat ggg ggc tgt gac gga aac agc aat aat tac ctg acc 540
 Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr
 65 70 75 80

aag gag gag tgc ctc aag aaa tgt gcc act gtc aca gag aat gcc acg 588
 Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr
 85 90 95

ggt gac ctg gcc acc agc agg aat gca gcg gat tcc tct gtc cca agt 636
 Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser
 100 105 110

gct ccc aga agg cag gat tct gaa gac cac tcc agc gat atg ttc aac 684
 Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn
 115 120 125

tat gaa gaa tac tgc acc gcc aac gca gtc act ggg cct tgc cgt gca 732
 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
 130 135 140

tcc ttc cca cgc tgg tac ttt gac gtg gag agg aac tcc tgc aat aac 780
 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
 145 150 155 160

ttc atc tat gga ggc tgc cgg ggc aat aag aac agc tac cgc tct gag 828
 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
 165 170 175

gag gcc tgc atg ctc cgc tgc ttc cgc cag cag gag aat cct ccc ctg 876
 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu
 180 185 190

ccc ctt ggc tca aag gtg gtg gtt ctg gcg ggg ctg ttc gtg atg gtg 924
 Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly Leu Phe Val Met Val
 195 200 205

ttg atc ctc ttc ctg gga gcc tcc atg gtc tac ctg atc cgg gtg gca 972
 Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala
 210 215 220

cgg agg aac cag gag cgt gcc ctg cgc acc gtc tgg agc tcc gga gat 1020
 Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp
 225 230 235 240

gac aag gag cag ctg gtg aag aac aca tat gtc ctg tgaccgcct 1066
 Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val Leu
 245 250

gtcgccaaga ggactgggga agggagggga gactatgtgt gagctttttt taaatagagg 1126

gattgactcg gatttgagtg atcattaggg ctgaggtctg tttctctggg aggtaggacg 1186
gctgcttctt ggtctggcag ggaatgggttt gctttggaaa tcctctagga ggctctctct 1246
cgcatggcct gcagctctggc agcagccccg agttgtttcc tcgctgatcg atttctttcc 1306
tccaggtaga gttttctttg cttatgttga attccattgc ctccttttct cnatcacaga 1366
agtgatgttg gaatcgtttc ttttgtttgt ctgatttatg gtttttttaa gtataaacia 1426
aagtttttta ttagcattct gaaagaagga aagtaaaatg tacaagttta ataaaaaggg 1486
gccttcccct ttagaataaa tttccagcat gttgctttca aaaaaaaaaa aaaaaaaa 1544

<210> 49
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)..(27)
<223>

<400> 49

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu
1 5 10 15

Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg
20 25 30

Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg
35 40 45

Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln
50 55 60

Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr
65 70 75 80

Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr
85 90 95

Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser
100 105 110

Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn
115 120 125

Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
130 135 140

Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
145 150 155 160

Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
165 170 175

Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu
180 185 190

Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly Leu Phe Val Met Val
195 200 205

Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala
210 215 220

Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp
225 230 235 240

Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val Leu
245 250

<210> 50
<211> 146
<212> PRT
<213> Homo sapiens

<400> 50

Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
1 5 10 15

Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
20 25 30

Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
35 40 45

Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr
50 55 60

Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln
65 70 75 80

Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys
85 90 95

Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp
100 105 110

Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly
115 120 125

Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu
130 135 140

Arg Cys
145

<210> 51
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> Consensus bikunin sequence of Fig. 4C.

<220>
<221> misc_feature
<222> (46)..(46)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (117)..(117)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (313)..(313)
<223> "n" is any nucleotide.

<400> 51
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tcgcaggcgg cgagggcgcg agtgaggagc agaccaggc atcgcgcgcc gagaagncgg 120

gcgtccccac actgaaggte cggaaaggcg acttccgggg gctttggcac ctggcggacc 180
 ctccccggagc gtcggcacct gaacgcgagg cgctccattg cgcggtgcgtt tgagggggctt 240
 cccgcacctg atcgcgagac cccaacggct ggtggcgctg ctgcgcgtct cggctgagct 300
 ggccatggcg cantgttgcg ggdtagggcg gacggcgttt ctgcctgct gggatcgctg 360
 ctctctctctg gggctctggc ggccgaccga gaacgcagca tccacgactt ctgcctgggtg 420
 tcgaagggtg tgggcagatg ccgggctctc atgcctaggt ggtggtacaa tgtcactgac 480
 ggatcctgcc agctgtttgt gtatgggggc tgtgacggaa acagcaataa ttacctgacc 540
 aaggaggagt gcctcaagaa atgtgccact gtcacagaga atgccacggg tgacctggcc 600
 accagcagga atgcagcgga ttctctctgtc ccaagtgtc ccagaaggca ggattctgaa 660
 gaccactcca gcgatatgtt caactatgaa gaatactgca ccgccaacgc agtcactggg 720
 ccttgccgtg catccttccc acgctggtac tttgacgtgg agaggaactc ctgcaataac 780
 ttcactctatg gaggtctccg gggcaataag aacagctacc gctctgagga ggcttgcgtg 840
 ctccgctgct tccgccagca ggagaatcct cccctgcccc ttgggtcaaa ggtgggtggtt 900
 ctggcggggc tgttcgtgat ggtgttgatc ctcttctctg gagcctccat ggtctacctg 960
 atccgggtgg cacggaggaa ccaggagcgt gccctgcgca ccgtctggag ctccggagat 1020
 gacaaggagc agctggtgaa gaacacatat gtctctgtgac cgccctgtcg ccaagaggac 1080
 tggggaaggg aggggagact atgtgtgagc tttttttaa tagagggatt gactcggatt 1140
 tgagtgatca ttagggctga ggtctgtttc tctgggaggt aggacggctg ctctctggtc 1200
 tggcagggat gggtttgctt tggaaatcct ctaggaggct cctcctcgca tggcctgcag 1260
 tctggcagca gccccagtt gtttctctgc tgatcgattt ctttctctca ggtagagttt 1320
 tctttgctta tgttgaattc cattgcctct tttctcatca cagaagtgat gttggaatcg 1380
 tttcttttgt ttgtctgatt tatggttttt ttaagtataa acaaaagttt tttattagca 1440
 ttctgaaaga aggaaagtaa aatgtacaag ttttaataaaa aggggccttc ccctttagaa 1500
 taataaaaaa aaaaaaaaaa aaaaaaaaaa 1530

<210> 52
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 52

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val

1 5 10 15

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
130 135 140

Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys
165 170

<210> 53
<211> 27
<212> PRT
<213> Homo sapiens

<400> 53

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu
1 5 10 15

Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala
20 25

<210> 54
<211> 23
<212> PRT
<213> Homo sapiens

<400> 54

Met Leu Arg Ala Glu Ala Asp Gly Val Ser Arg Leu Leu Gly Ser Leu
1 5 10 15

Leu Leu Ser Gly Val Leu Ala
20

<210> 55
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' sense oligonucleotide used for construct #2 in Example 5.

<400> 55
gaaggggtaa gcttggataa aagagaagaa tactgtactg ctaatgctgt tactgggtcca 60
tgtagagctt cttttccaag atggtacttt gatgttgaaa ga 102

<210> 56
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' antisense oligonucleotide used for construct #2 in Example 5.

<400> 56
actggatcct cattggcgaa aacatctcaa catacaggct tcttcagatc tgtaagaatt 60
tttattacct ctacaaccac cgtaaataaa attattacaa gaatttcttt caacatcaaa 120
gtaccatct 129

<210> 57
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' sense oligonucleotide used for construct #3 in Example 5.

<400> 57
gaaggggtaa gcttggataa aagaaattac gaagaatact gtactgctaa tgctgttact 60

gggccatgta gagcttcttt tccaagatgg tactttgatg ttgaaaga 108

<210> 58
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' sense oligonucleotide used for construct #4 in Example 5.

<400> 58
gaaggggtaa gcttggataa aagagatatg ttttaattacg aagaatactg tactgctaata 60

gctgttactg gtccatgtag agcttctttt ccaagatggg actttgatgt tgaaaga 117

<210> 59
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Sense oligonucleotide used in PCR in Example 8.

<400> 59
cacctgatcg cgagacccc 19

<210> 60
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense oligonucleotide used in PCR in Example 8.

<400> 60
ctggcggaag cagcggagca tgc 23

<210> 61
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide used in in vitro mutagenesis in Example 9.

<400> 61
cgcgtctcgg ctgacctggc cctgcagatg ggcacgtgt gcggg 45

<210> 62
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide used in in vitro mutagenesis in Example 9.

<400> 62

ctgccccttg gctcaaagta ggaagatctt ccccccgggg gggtaggttct ggcggggctg 60

<210> 63

<211> 14

<212> PRT

<213> Homo sapiens

<400> 63

Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Pro Leu Gly
1 5 10

<210> 64

<211> 20

<212> PRT

<213> Homo sapiens

<400> 64

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
1 5 10 15

Val Gly Arg Cys
20

<210> 65

<211> 20

<212> PRT

<213> Homo sapiens

<400> 65

Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys
1 5 10 15

Arg Ala Ser Phe
20

<210> 66

<211> 11

<212> PRT

<213> Homo sapiens

<400> 66

Pro Arg Tyr Val Asp Gly Ser Gln Phe Tyr Gly

1

5

10

<210> 67
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 67

Val Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
 1 5 10 15

Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu
 20 25 30

Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu
 35 40 45

Val Lys Asn Thr Tyr Val Leu
 50 55

<210> 68
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 68

Val Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
 1 5 10 15

Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu
 20 25 30

Arg Ala Leu Arg Thr Val Trp Ser Phe Gly Asp
 35 40

<210> 69
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 69

Val Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
 1 5 10 15

Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu

20 25 30
 Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu
 35 40 45
 Val Lys Asn Thr Tyr Val Leu
 50 55
 <210> 70
 <211> 213
 <212> PRT
 <213> Homo sapiens
 <400> 70
 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
 1 5 10 15
 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
 20 25 30
 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
 35 40 45
 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
 50 55 60
 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
 65 70 75 80
 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
 85 90 95
 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
 100 105 110
 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
 115 120 125
 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
 130 135 140
 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
 145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
165 170 175

Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr
180 185 190

Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
195 200 205

Trp Ser Phe Gly Asp
210

<210> 71
<211> 225
<212> PRT
<213> Homo sapiens

<400> 71

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
1 5 10 15

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn

130 135 140
 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
 145 150 155 160
 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
 165 170 175
 Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr
 180 185 190
 Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
 195 200 205
 Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val
 210 215 220
 Leu
 225

<210> 72
 <211> 19
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> "Xaa" is Ile, Thr, Asn, or Ser.

<220>
 <221> MISC_FEATURE
 <222> (11)..(11)
 <223> "Xaa" is Val, Ala, Glu, or Gly.

<220>
 <221> MISC_FEATURE
 <222> (17)..(17)
 <223> "Xaa" is Ser, Pro, Thr, or Ala.

<220>
 <221> MISC_FEATURE
 <222> (19)..(19)
 <223> "Xaa" is Tyr, His, Asn, or Asp.

<400> 72

Arg Pro Leu Gln Arg Tyr Val Ser Xaa Ile Xaa Arg Ile Ile Ala Pro
1 5 10 15

Xaa Thr Xaa

<210> 73
<211> 108
<212> PRT
<213> Homo sapiens

<400> 73

Pro Gly His Gln Gln Glu Cys Ser Gly Phe Leu Cys Pro Lys Ser Pro
1 5 10 15

Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr Glu
20 25 30

Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe
35 40 45

Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile
50 55 60

Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala
65 70 75 80

Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu Pro Leu
85 90 95

Gly Ser Lys Val Val Val Leu Ala Gly Ala Val Ser
100 105

<210> 74
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> "Xaa" is Asp or Glu.

<400> 74

Ser Phe Ser Trp Gly Ala Ser Met Val Leu Leu Ile Pro Gly Gly Lys
1 5 10 15

Glu Glu Pro Gly Ala Cys Pro Ala Xaa Arg Leu Glu Leu Arg Arg
20 25 30

<210> 75
<211> 511
<212> DNA
<213> Artificial Sequence

<220>
<223> Corrected version of EST R74593 (see Fig. 3 and page 28).

<220>
<221> misc_feature
<222> (425)..(425)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (482)..(482)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (510)..(510)
<223> "n" is any nucleotide.

<400> 75
gcaataatta cctgaccaag gaggagtgcc tcaagaaatg tgccactgtc acagagaatg 60
ccacgggtga cctggccacc agcaggaatg cagcggattc ctctgtccca agtgctccca 120
gaaggcagga ttctgaagac cactccagcg atatgttcaa ctatgaagaa tactgcaccg 180
ccaacgcagt cactgggcct tgccgtgcat ccttcccacg ctggtacttt gacgtggaga 240
ggaactcctg caataacttc atctatggag gctgccgggg caataagaac agctaccgct 300
ctgaggaggc ctgcatgtc cgctgcttcc gccagcagga gaatcctccc ctgcccttg 360
gctcaaaggt ggtggttctg gccggggctg tttcgtgatg gtgttgatcc ttttctggg 420
gagcntccat ggtcttactg attcgggtg gcaaggagga accaggagcg tgcctgagg 480
ancgtctgga gcttcggaga tgacaaggn t 511

<210> 76
<211> 31
<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acids 184-214 of translation of consensus sequence in Fig. 3.

<220>

<221> MISC_FEATURE

<222> (25)..(25)

<223> "Xaa" is Asp or Glu.

<400> 76

Ser Phe Ser Trp Gly Ala Ser Met Val Leu Leu Ile Pro Gly Gly Lys
1 5 10 15

Glu Glu Pro Gly Ala Cys Pro Ala Xaa Arg Leu Glu Leu Arg Arg
20 25 30

<210> 77

<211> 312

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (45)..(45)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (49)..(49)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (118)..(118)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (231)..(231)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (305)..(305)

<223> "n" is any nucleotide.

<400> 77

gcgacctccg cgcgttgga ggtgtagcgc ggctctgaac gcgtngagng gccgttgagt 60
 gtcgcaggcg gcgagggcgc gaggtaggag cagaccagg catcgcgcc cgagaagncg 120
 ggcgtcccca cactgaaggt cggaaaggc gacttcggg ggctttggca cctggcggac 180
 cctcccgag cgtcggcacc tgaacgcgag gcgtccatt gcgcgtgcgt ntgaggggct 240
 tcccgacct gatcgcgaga cccaacggc tgggtggcgc gcctgcgcgt ctcggctgag 300
 ctggncatgt cg 312

<210> 78
 <211> 330
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (117)..(117)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (123)..(123)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (321)..(321)
 <223> "n" is any nucleotide.

<400> 78
 gcgacctccg cgcgttgga ggtgtagcgc ggctctgaac gcgtgcaggg ccgttgagtg 60
 tcgcaggcg cgagggcgc agtgaggagc agaccaggc atcgcgccc gagaagncg 120
 gntccccac actgaaggtc cggaaaggc acttcgggg gctttggcac ctggcggacc 180
 ctcccgagc gtggcacctg aacgcgaggc gctccattgc gcgtgcgttt gaggggcttc 240
 ccgcacctga tcgcgagacc ccaacggctg gtggcgtcgc ctgcgcgtct cggctgagct 300
 ggccatggcg cactgtgcgg nctgaggcg 330

<210> 79
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (9)..(9)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (11)..(11)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (222)..(222)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (231)..(231)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (262)..(262)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (267)..(274)
<223> "n" is any nucleotide.

<400> 79
ttgagtgtng naggcggcga gggcgcgagt gaggagcaga cccaggcatc gcgcgccgag 60
aaggccgggc gtccccacac tgaaggctcg gaaaggcgac ttccgggggc tttggcacct 120
ggcggaccct cccggagcgt cggcacctga acgcgaggcg ctccattgcg cgtgcgtttg 180
aggggcttcc cgcacctgat cggagagacc caacggctgg tngcgtcgct ncgcgtctcg 240
gctgagcttg gccatggcgc antgttnccg gctnaggcgg acg 283

<210> 80
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (44)..(44)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (46)..(46)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (76)..(76)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (114)..(114)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (187)..(187)
<223> "n" is any nucleotide.

sub <220>
<221> misc_feature
<222> (268)..(268)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (309)..(309)
<223> "n" is any nucleotide.

*as
CNT* <220>
<221> misc_feature
<222> (317)..(317)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (332)..(332)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (370)..(370)
<223> "n" is any nucleotide.

<400> 80
ggcgacctcc ggcggttggg aggtgtagcg cgctctgaac gggngangggc cgttgagtgt

60

cgcagcgccg agggcngagt gaggagcaga cccagggcatc gcgcgcccag aagncggggcg 120
 tccccacact gaaggtccgg aaagggcgact tccggggggct ttggcacctg gcggacgtcc 180
 cggagcnggc acctgaacgc gaggcgctcc attgcgcgtg cgtttgaggg gcttcccgca 240
 cctgatcgcg agaccccaac ggctggtngc gtcgctggcg cgttctcggc tgagctggcc 300
 atggcgcant gttgcgngct gagggcgacc gncgtttttc ttcgccttgc tgggattcgc 360
 ttgcttccn tctggggggt cctggggcggc cgaccgagaa cgcagcatcc aagaattttt 420
 gcc 423

<210> 81
 <211> 344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (35)..(35)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (148)..(148)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (235)..(235)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (261)..(261)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (272)..(272)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (293)..(293)
 <223> "n" is any nucleotide.

<220>

<221> misc_feature
<222> (300)..(300)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (313)..(313)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (320)..(320)
<223> "n" is any nucleotide.

<400> 81
ggaggagcag acccagggcat cgcgcgccga gaagncgggc gtccccacac tgaagggtccg 60
gaaaggcgac ttccgggggc tttggcacct ggccggaccct cccggagcgt cggcacctga 120
acgcgaggcg ctccattgcg cgtgcgtntg gaggggcttc ccgcacctga tcgcgagacc 180
ccaacggctg gtggggcgctg ctgcgcgtct tcggctgagc tgggccatgg cgcanttggt 240
gcgggctgag gccggacgcgg ncgttttttc gnccttgetg ggattcggtg ttncctctctn 300
gggggttctgg ggngggccgan cgagaacgca agcattcacg attt 344

<210> 82
<211> 253
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (56)..(56)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (137)..(137)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (145)..(145)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (159)..(159)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (233)..(233)

<223> "n" is any nucleotide.

<400> 82

ggaccctccc ggagcgtcgg cacctgaacg cgaggcctcc attgcggtgc gtgtgnaggg 60

gcttcccgca cctgatcgcg agaccccaac ggctggtggc gtcgctgcgc gtctcggtcg 120

agctggccat ggcgcantgt tgcgngctga ggcggcggnc gttttctcgc ctgctgggat 180

cgctgctcct ctctgggggc ctggcggccg accgagaacg cagcatccac gantttcttc 240

tggtgttcga agg 253

<210> 83

<211> 419

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (20)..(20)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (26)..(26)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (95)..(95)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (292)..(292)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (313)..(315)

<223> "n" is any nucleotide.

<400> 83

ttagcgcggc tctgaacgcn agaagnggcc gttgagtgtc gcaggcggcg agggcgcgag 60
 tgaggagcag acccagggcat cgcgcgccga gaagncgggc gtccccacac tgaagggtccg 120
 gaaaggcgac ttccgggggc tttggcacct ggcggaccct cccggagcgt cggcacctga 180
 acgcgaggcg ctccattgcy cgtgcggttg aggggcttcc cgcacctgat cgcgagaccc 240
 caacggctgg tggcgctgcc tgcgcgtctc ggctgagctg gccatggcgc antggtgcgg 300
 gcttgaggcg gannngcgt ttctgcctg ctgggatcgc tgctcctctc tgggggtcctg 360
 gcggccgacc gagaacgcag catccacgac ttctgcctgg tgtcgaaggt ggtgggcag 419

<210> 84
 <211> 477
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (27)..(27)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (139)..(139)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (223)..(223)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (232)..(232)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (302)..(302)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (310)..(310)
 <223> "n" is any nucleotide.

<220>

<221> misc_feature
<222> (322)..(322)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (328)..(328)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (357)..(357)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (375)..(375)
<223> "n" is any nucleotide.

but B6
<220>
<221> misc_feature
<222> (392)..(392)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (398)..(398)
<223> "n" is any nucleotide.

*AS
cont*
<220>
<221> misc_feature
<222> (405)..(405)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (427)..(427)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (437)..(437)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (449)..(449)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (458)..(458)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (474)..(474)
<223> "n" is any nucleotide.

<400> 84
agacccaggc atcgcgcgcc gagaagncgg gcgtcccccac actgaaggtc cggaaaggcg 60
acttccgggg gctttggcac ctggcggaacc ctcccggagc gtcggcacct gaacgcgagg 120
cctccattgc cgtgcgttng aggggcttcc cggaacttga tcgcgagacc ccaacggctg 180
gtggcgctgc tgcgcgtcct cggctgagct ggccatggcg cantggtgcc gngctgaggc 240
cggagggccg gtttctcgcc ttgctgggat cgctgctcct ctctggggtc ctggcggccg 300
ancgaagaan gcagcaatcc angaatttct gcctgggtgtt cgaaagttgg tgggcanatt 360
ccggggcctt catgnctaag gttggttggg anaatgtnaa ttaangattc ttgcaactgt 420
ttgtgtgnatt ggggctntta aacggaaana caataatnac ctgaccaaag aagnaatt 477

<210> 85
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (361)..(361)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (367)..(367)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (384)..(384)
<223> "n" is any nucleotide.

<220>
<221> misc_feature

<222> (390)..(390)
<223> "n" is any nucleotide.

<400> 85
ggccgggtcg tttctcgctt ggctgggata gctgctcttc tctgggggtcc tggccgggccg 60
accgagaacg cagcatccac gacttctgcc tgggtgtcgaa ggtgggtgggc agattccggg 120
cctccatgcc taggtgggtg tacaatgtca ctgacggata ctgccagctg tttgtgtatg 180
ggggctgtga cggaaacagc aataattacc tgaccaagga ggagtgcctc aagaaatgtg 240
ccactgtcac agagaatgcc acgggtgacc tggccaccag caggaatgca gcggattcct 300
ctgtcccaag tgctcccaga aggcaggatt cttgaagacc acttcagcga tatgtttcaa 360
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<210> 86
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<213> Homo sapiens

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agaacgcagc atccacgact tctgcctggt gtcgaagggt gtgggcagat gccgggcctc 120
catgcctagg tgggtgtaca atgtcactga cggatcctgc cagctgtttg tgtatggggg 180
ctgtgacgga aacagcaata attacctgac caaggaggag tgcctcaaga aatgtgccac 240
tgtcacagag aatgccacgg gtgacctggc caccagcagg aatgcagcgg attcctctgt 300
cccaagtgt cccagaaggc aggattctga agaccactcc agcgatatgt tcaactatga 360
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<210> 87
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<400> 87
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caatgtcact gacggatcct gccagctgtt tgtgtatggg ggctgtgacg gaaacagcaa 180
taattacctg accaaggagg agtgcctcaa gaaatgtgcc actgtcacag agaatgccac 240
gggtgacctg gccaccagca ggaatgcagc ggattcctct gtcccaagtg ctcccagaag 300
gcaggattct gaagaccact ccagcgatat gttcaactat gaagaatact gcaccgcca 360
cgcagtcact ggggccttgc gtggaatcct tccccacgct ggnaatttng acgttgagaa 420
ggaac 425

<210> 88
<211> 343
<212> DNA
<213> Homo sapiens

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<223> "n" is any nucleotide.

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<222> (211)..(211)
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Pub 86
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<222> (245)..(245)
<223> "n" is any nucleotide.

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<223> "n" is any nucleotide.

<220>
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ctctgtccca agtgctccca gaaggcagga ttctgaagac cactccagcg atatgttcaa 180
ctatgaagaa tactgcaccg ccaacgcagt nactggggcc ttgcgtggca tnccttccca 240
cgctngtact ttgacgtgga gaggaactcc tggcaataac ttcatttatg gaggcttgcc 300

ggggcaatna agaacagntt accgctcttt aggaggcctg cat

343

<210> 89
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<212> DNA
<213> Homo sapiens

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<223> "n" is any nucleotide.

<220>
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<222> (509)..(509)
<223> "n" is any nucleotide.

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ccacgggtga cctggccacc agcaggaatg cagcggattc ctctgtccca agtctcccag 120
aaggcaggat tctgaagacc actccagcga tatgttcaac tatgaagaat actgcaccgc 180
caacgcagtc actgggcctt gccgtgcac cttcccacgc tgggtactttg acgtggagag 240
gaactcctgc aataacttca tctatggagg ctgccggggc aataagaaca gctaccgctc 300
tgaggaggcc tgcattgtcc gctgcttccg ccagcaggag aatcctcccc tgccccttgg 360
ctcaaagggtg gtggttcttg ccggggctgt ttcgtgatgg tgttgatcct tttcctgggg 420
agcntccatg gtcttactga ttccgggtgg caaggaggaa ccaggagcgt gccctgcgga 480
ncgtctggag cttcggagat gacaaggnt 510

<210> 90
<211> 293
<212> DNA
<213> Homo sapiens

<220>
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<222> (257)..(257)
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<400> 90
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tgccccttgg ctcaaaggtg gtggttctgg cggggctggt cgtgatggtg ttgatcctct 120
tcctggggag cctccatggt ctacctgac cgggtggcac ggagggaacc agggagcgtg 180
ccctgcgcac cgtctgggag ctccggagat gacaaggag cagctgggtg aagaacacat 240
atgttctctgt tgaccgncct gttcgccaag aggattgggg gaaggagggg gga 293

<210> 91
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<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (147)..(147)
<223> "n" is any nucleotide.

<400> 91
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gggctgttcg tgatggtggt gatccctcct tcccgggagc ctcccatggt cctaccctga 120
tccgggtggc acggagggaac ccaggancgt gccctgcgca ccgtctggag ctccggagat 180
gacaaggagc agctggtgaa gaacacatat gtcctgtgac cgccctgtcg ccaagaggac 240
tggggaaggg aggggagact atgtgtgagc tttttttaaa ta 282

<210> 92
<211> 390
<212> DNA
<213> Homo sapiens

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<220>
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<222> (55)..(55)
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Sub-B6
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<223> "n" is any nucleotide.

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<223> "n" is any nucleotide.

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gagaatcctc cctgcccct tggctcaaag gtggtggttc tggcggggct gttcgtgatg 180
gtgttgatcc tcttctctggg agcctccatg gtntacctga tccgggtngc acggaggaac 240
cagggagcgt gccctgcgna ccgtctngga gctccggaga tgacaaggag cagctggtga 300
agaacacata tgtcctgtga ccgcctggt cgncaagagg actnggggaa aggggagggg 360
agattatgtg ttgagttttt tttaaantag 390

<210> 93
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<223> "n" is any nucleotide.

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tccgctgctt ccgccagcag gagaatcctc cctgcccct tggctcaaag gtggtgggtc 120
tggcggggct gttcgtgatg gtgttgatcc tcttctggg agcctccatg gtctacctga 180
tccgggtggc acggaggaac caggagcgt gccctgcgca ccgtctggga gctccggaga 240
tgacaaggga gcagctggtg aagaacacat atgttctgt tgaccgccct gttcgccaag 300
agggantggg ggaaggggag ggggaganta ttgttggtga gntttttttt aaaattagga 360
ggggnttgan ttcgggnttt tnagttgatc catttagggg gntgag 406

<210> 94
<211> 360
<212> DNA
<213> Homo sapiens

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<220>
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<222> (339)..(339)
<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (347)..(347)
<223> "n" is any nucleotide.

<400> 94

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 catggtctac ctgatccggg tngcacggag gaaccaggag cgtgccctgc gcaccgtctg 180
 gagctccgga gatgacaagg agcagctggt gaagaacaca tatgtcctgt gaccgcctg 240
 tcgccaagag gactggggaa gggaggggag actatgtgtg agcttttttt aaatagaggg 300
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<210> 95
 <211> 438
 <212> DNA
 <213> Homo sapiens

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 <223> "n" is any nucleotide.

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 <223> "n" is any nucleotide.

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 <223> "n" is any nucleotide.

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 ggggtggcacg gaggaaccag gacgctgcc tgccgaccgt ctggagctcc ggagatgaca 120
 aggagcagct ggtgaagaac acatatgtcc tgtgaccgcc ctgtcgccaa gaggactggg 180
 gaagggaggg gagactatgt gtgagcttct tttaaataga gggattgact cggatttgag 240
 tgatcattag ggctgaggtc tgtttctctg ggaggtagga cggctgcttc ctgggtcttg 300
 gcagggatgg ggtttgcttt gggaaatcct cttnngaggc tcctccttcg catgggcctt 360
 gcagtctngg cagcancccc cgagtttttt tccttcgctg atccgatttc ttttctcca 420
 ggtaagaatt tttctttt 438

<210> 96
 <211> 448
 <212> DNA

<213> Homo sapiens

<220>

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<222> (108)..(108)

<223> "n" is any nucleotide.

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<221> misc_feature

<222> (261)..(261)

<223> "n" is any nucleotide.

<400> 96

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ggtgaagaac acatatgtcc tgtgaccgcc ctgtcgccaa gaggactngg gaagggaggg 120

gagactatgt gtgagctttt tttaaataga gggattgact cggatttgag tgatcattag 180

ggctgaggtc tgtttctctg ggaggttagga cggctgcttc ctggtctggc agggatgggt 240

ttgctttgga gaatcctcta ngaggctcct cctcgcatgg cctgcagtct ggcagcagcc 300

ccgagttggt tctctgctga tctgatttctt tctccaggt agagttttct ttgcttatgt 360

tgaattccat tgctctttt ctcacacag aagtgatgtt ggaatcgttt cttttgtttt 420

gtctgattta tgggtttttt ttaagtat 448

<210> 97

<211> 331

<212> DNA

<213> Homo sapiens

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<222> (30)..(30)

<223> "n" is any nucleotide.

<400> 97

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atggggtttgc tttggaaatc ctctaggagg ctctcctctg catggcctgc agttctgcag 120

cagccccgag ttgtttcttc gctgatcgat ttctttcttc caggtagagt tttctttgct 180

tatgttgaat tccattgcct cttttctcat cacagaagtg atgttggaat cgtttctttt 240

gtttgtctga tttatgggtt ttttaagtat aaacaaaagt tttttattag cattctgaaa 300

gaaggaaagt aaaatgtaca agtttaataa a 331

<210> 98
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<212> DNA
<213> Homo sapiens

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sub B.
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<220>
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<222> (337)..(337)
<223> "n" is any nucleotide.

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gctgctcccc tggctctggca gggatggggtt tgctttggaa anccnctagg aggctcctcc 120

tcgcatggcc tgcagtctgg cagcagcccc gagttgttnc ctcgctgac gatntctttc 180
 ccccaggtag agttttcttt gcttatgttg aantccattg cctcttttct catcacagaa 240
 gtgatgttgg aatcgtttct tttgtttgtc tgatttatgg tttttttaag tataaacaac 300
 agttttttat tagcattctg aaagaaggaa agtaaatgt acaagtttaa taaaaagggg 360
 ccttccccct taa 373

<210> 99
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 99
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 ggctgcttcc tggctctggca gggatgggtt tgctttggaa atcctctagg aggctcctcc 120
 ttgcatggc ctgcagtctg gcagcagccc cgagttgttt ctcgctgat cgatttcttt 180
 cctccaggtg gagttttctt tgcttatgtt gaattccatt gcctcttttc tcatcacaga 240
 agtgatgttg gaatcgtttc tttgtttgt ctgatttatg gtttttttaa gtataaaca 300
 aagtttttta ttagcattct gaaagaagga aagtaaaatg tacaagttta ataaaaaggg 360
 gccttccccct ttagaataaa 380

<210> 100
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (304)..(304)
 <223> "n" is any nucleotide.

<220>
 <221> misc_feature
 <222> (309)..(309)
 <223> "n" is any nucleotide.

<400> 100
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 agtctggcag cagcccaggt tgtttctcgc ctgatcgatt tctttcctcc aggtagagtt 120
 ttctttgctt atgttgaatt ccattgctc ttttctcatc acagaagtga tgttggaatc 180

gtttcttttg tttgtctgat ttatggtttt ttttaagtata aacaaaagtt ttttattagc 240
 attctgaaag aaggaaagta aaatgtacaa gtttaataaa aaggggcctt ccccttttagg 300
 aatnaaaaana aaaaagggtg 320

<210> 101
 <211> 397
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> "n" is any nucleotide.

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 tcgcatggcc tgcagtctgc agcagcccg agttgtttcc tcgctgatcg atttctttcc 180
 tccaggtaga gttttctttg cttatgttga attccattgc ctcttttctc atcacagaag 240
 tgatgttggga atcgtttctt ttgtttgtct gatttatggg ttttttaagt ataaacaaaa 300
 gttttttatt agcattctga aagaaggaaa gtaaaatgta caagtttaat aaaaaggggc 360
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<210> 102
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 <222> (74)..(74)
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<220>
 <221> misc_feature
 <222> (122)..(122)
 <223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (184)..(184)
<223> "n" is any nucleotide.

<400> 102
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nccgatttctt tccnccaggt agagttttct ttgcttatgt tgaattccat tgcctctttt 120
cncatcacag aagtgatgtt ggaatcgttt cttttgtttg tctgatttat ggttttttta 180
agtntaaaca aaagtttttt attagcattc tgaaagaagg aaagtaaaat gtacaagttt 240
aataaaaagg ggccttcccc tttagaataa aaaaaaaaaa aaaaaaaaaa 289

<210> 103
<211> 311
<212> DNA
<213> Homo sapiens

<220>
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<222> (7)..(7)
<223> "n" is any nucleotide.

<400> 103
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attccattgc ctcttttctc atcacagaag tgatgttgga atcgtttctt ttgtttgtct 180
gatttatggg ttttttaagt ataaacaaaa gttttttatt agcattctga aagaaggaaa 240
gtaaaatgta caagtttaat aaaaaggggc cttccccttt agaataaatt tcagcatgtg 300
ctttcaaaaa a 311

<210> 104
<211> 338
<212> DNA
<213> Homo sapiens

<220>
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<223> "n" is any nucleotide.

<220>
<221> misc_feature
<222> (67)..(67)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (136)..(136)

<223> "n" is any nucleotide.

<400> 104

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tgcagtnctg gcagcagacc ccgagttggt tctctgctga tcgatttctt taccctcagg 120

tagagttttc ctttgnctta tgttgaattc cattgcctct tttactcatc acagaagtga 180

tgttggaaac gtttcttttg tttgtctgat ttatgggttt ttttaagtata aacaaaagtt 240

ttttattagc attctgaaag aaggaaagta aaatgtacaa gtttaataaa aaggggcctt 300

cccttttaga ataaaaaaaa aaaaaaaaaa aaaaaaaaa 338

<210> 105

<211> 343

<212> DNA

<213> Homo sapiens

<220>

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<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (19)..(19)

<223> "n" is any nucleotide.

<220>

<221> misc_feature

<222> (107)..(107)

<223> "n" is any nucleotide.

<400> 105

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ccaggtagag ttttctttgc ttatgttgaa ttccattgcc tcttttctca tcacagaagt 180

gatgttgga tcttttcttt tgtttgtctg atttatgggt tttttaagta taaacaaaag 240

ttttttatta gcattctgaa agaaggaaag taaaatgtac aagtttaata aaaaggggcc 300

But B6
Q5
CMT

ttccccttta gaataaaaaa aaaaaaaaaa aaaaaaaaaa aaa

343